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Abstracts, 5th DICID

State-of-the Art Lecture 1

Friday, July 15, 2011, 08:30–09:00
Meeting Room 309

SOTA1 Hospital Setting: Infection control in the resistance era

W.-H. Seto*. *WHO Collaborating Centre for Infection Control, Hong Kong S.A.R.*

In the hospital, for infection control, it is generally recognized that it is easier to prevent the spread of Gram-negative organisms as compared to the Gram positive bacteria. A summary of the study by Lemmen et al, JHI 2004:56:191–197 and data from Queen Mary Hospital Hong Kong will be presented to support the concept. The MDR Gram-negative organisms are now the focus of global attention. A brief review of the different types and their epidemiology in Asia will be presented. A two-tier system for infection control of MDROs is generally recommended as also by the CDC of USA. The system will be described. In the second tier of preventive measures, the particular measures must be selected based on the organism. In terms of the newer Gram-negative MDROs, this can be difficult because the epidemiology of the organisms is still not entirely clear. Furthermore the effectiveness of the different microbiology methods such as for screening and surveillance is not well defined. Nevertheless an attempt will be made to present the best possible strategies for various Gram-negative organisms in the present context.

Concurrent Session 1: Hepatitis C – Discovering Genomics

Friday, July 15, 2011, 09:15–10:45
Meeting Room 310

CS1.1 HCV genotypes in hepatitis C patients and their clinical significances

J. Cheng*. *Capital University Affiliated Beijing Ditan Hospital, China*

Abstract not available

CS1.2 Hepatitis C pharmacogenetics

G. Ahlenstiel*. *Storr Liver Unit, Westmead Millennium Institute, Westmead Hospital, University of Sydney, Westmead, Australia*

Traditionally, the candidate gene approach has been the standard pharmacogenetic method to identify genetic polymorphisms relevant for treatment response in human disease. In 2009 this changed forever, when four independent groups employed genome wide association studies (GWAS) to examine the response to interferon-alpha and ribavirin treatment of chronic hepatitis C virus (HCV) genotype 1 infection. Importantly, all four studies consistently identified polymorphisms in the interleukin 28B (IL28B) gene, a lambda interferon, as a major determinant of treatment outcomes. This represented a breakthrough for our understanding of the pathogenesis of HCV infection and in drug response for chronic hepatitis C. The studies have identified IL28B as a pivotal molecule in these contexts and explain to some degree the differences between ethnic groups in treatment responses and the mechanisms for spontaneous HCV clearance. More recent studies have addressed the role of IL28B polymorphisms in the natural history of HCV infection as well as in the context of HCV genotype 2 and 3 disease and in liver transplantation. This presentation is an update on the current understanding of the role of IL28B in HCV infection as well as the role of GWAS in HCV pharmacogenetics.

CS1.3 Genomic-based treatment paradigms for patients with chronic hepatitis C infection

A.J. Thompson*. *Head of Hepatology Research, St Vincent's Hospital, NHMRC Research Fellow, University of Melbourne, Research Fellow, Victorian Infectious Diseases Reference Laboratory (VIDRL) & Honorary Visiting Assistant Professor, Duke University Medical Center, Melbourne, Australia*

Abstract not available

CS1.4 Association of IL28B gene variations with mathematical modeling of viral kinetics in chronic hepatitis C patients

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Background and Aims: Asian chronic hepatitis C (CHC) patients are known to have better virologic responses to pegylated interferon-based therapy than Western patients. Although IL28B gene polymorphisms may contribute to this difference, whether favorable hepatitis C virus (HCV) kinetics during treatment also plays a role remains unclear. Therefore, we conducted this study to explore the